

Sequence Listing

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Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
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Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val
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GIKAIAEYKV YTAGEAIDLL HYVAPKMMAR GAAHFSYGIN DDLDDETKYQD 500
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FTSAHEEDED SCLKAGVYNV DGDETVPVLS AGYMCAKAWR GKTRFNPNSGI 600
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Trp Arg Gly Lys Thr Arg Phe Ser Pro Ala Gly Ser Lys Thr Tyr Val
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Thr Gln Ser Gly Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile
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GAG GAC GTC ATC AGA ATA GCT GCT GGG GCA ACC GGT GAG GAA ATT GGT 288
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 100 105 110

15 Ser Phe Gln Asn Thr Glu Arg Asp Gln Thr Leu Ser Arg Met Lys Ser
 115 120 125

20 Asn Ile Glu Leu Met Val Ser Thr Asn Gly Gly Lys Lys Ala Val Ile
 130 135 140

Val Pro His Ser Met Gly Val Leu Tyr Phe Leu His Phe Met Lys Trp
 145 150 155 160

25 Val Glu Ala Pro Ala Pro Leu Gly Gly Gly Pro Asp Trp Cys
 165 170 175

Ala Lys Tyr Ile Lys Ala Val Met Asn Ile Gly Gly Pro Phe Leu Gly
 180 185 190

30 Val Pro Lys Ala Val Ala Gly Leu Phe Ser Ala Glu Ala Lys Asp Met
 195 200 205

Arg Met Thr Arg Thr Trp Asp Ser Thr Met Ser Met Leu Pro Lys Gly
 210 215 220

Gly Asp Thr Ile Trp Gly Gly Leu Asp Trp Ser Pro Glu Leu Pro Asn
 225 230 235 240

40 Ala Pro Glu Met Glu Ile Tyr Ser Leu Tyr Gly Val Gly Ile Pro Thr
 245 250 255

Glu Arg Ala Tyr Val Tyr Lys Leu Asn Gln Ser Pro Asp Ser Cys Ile
 260 265 270

45 Pro Phe Gln Ile Phe Thr Ser Ala His Glu Glu Asp Glu Asp Ser Cys
 275 280 285

50 Leu Lys Ala Gly Val Tyr Asn Val Asp Gly Asp Glu Thr Val Pro Val
 290 295 300

Leu Ser Ala Gly Tyr Met Cys Ala Lys Ala Trp Arg Gly Lys Thr Arg
 305 310 315 320

55 Phe Asn Pro Ser Gly Ile Lys Thr Tyr Ile Arg Glu Tyr Asn His Ser
 325 330 335

Pro Pro Ala Asn Leu Leu Glu Gly Arg Gly Thr Gln Ser Gly Ala His
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60 Val Asp Ile Met Gly Asn Phe Ala Leu Ile Glu Asp Ile Met Arg Val

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25	gat gaa aac aat aaa ggg ggt tct gtt cat aac aag cga gag agc aga Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg 20 25 30 35			96
30	aac cac att cat cat caa cag gga tta ggc cat aag aga aga agg ggt Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly 35 40 45			144
35	att agt ggc agt gca aaa aga aat gag cgt ggc aaa gat ttc gac agg Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg 50 55 60			192
40	aaa aga gac ggg aac ggt aga aaa cgt tgg aga gat tcc aga aga ctg Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu 65 70 75 80			240
45	att ttc att ctt ggt gca ttc tta ggt gta ctt ttg ccg ttt agc ttt Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe 85 90 95			288
50	ggc gct tat cat gtt cat aat agc gat agc gac ttg ttt gac aac ttt Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe 100 105 110			336
55	gta aat ttt gat tca ctt aaa gtg tat ttg gat gat tgg aaa gat gtt Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val 115 120 125			384
60	ctc cca caa ggt ata agt tcg ttt att gat gat att cag gct ggt aac Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn 130 135 140			432
	tac tcc aca tct tct tta gat gat ctc agt gaa aat ttt gcc gtt ggt Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly 145 150 155 160			480
	aaa caa ctc tta cgt gat tat aat atc gag gcc aaa cat cct gtt gta Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val			528

	165	170	175	
5	atg gtt cct ggt gtc att tct acg gga att gaa agc tgg gga gtt att Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile 180 185 190			576
10	gga gac gat gag tgc gat agt tct gcg cat ttt cgt aaa cgg ctg tgg Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp 195 200 205			624
15	gga agt ttt tac atg ctg aga aca atg gtt atg gat aaa gtt tgt tgg Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp 210 215 220			672
20	ttg aaa cat gta atg tta gat cct gaa aca ggt ctg gac cca ccg aac Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn 225 230 235 240			720
25	ttt acg cta cgt gca gca cag ggc ttc gaa tca act gat tat ttc atc Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile 245 250 255			768
30	gca ggg tat tgg att tgg aac aaa gtt ttc caa aat ctg gga gta att Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile 260 265 270			816
35	ggc tat gaa ccc aat aaa atg acg agt gct gcg tat gat tgg agg ctt Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu 275 280 285			864
40	gca tat tta gat cta gaa aga cgc gat agg tac ttt acg aag cta aag Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys 290 295 300			912
45	gaa caa atc gaa ctg ttt cat caa ttg agt ggt gaa aaa gtt tgt tta Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu 305 310 315 320			960
50	att gga cat tct atg ggt tct cag att atc ttt tac ttt atg aaa tgg Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp 325 330 335			1008
55	gtc gag gct gaa ggc cct ctt tac ggt aat gat ggt cgt ggc tgg gtt Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Arg Gly Trp Val 340 345 350			1056
60	aac gaa cac ata gat tca ttc att aat gca gca ggg acg ctt ctg ggc Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly 355 360 365			1104
	gct cca aag gca gtt cca gct cta att agt ggt gaa atg aaa gat acc Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr 370 375 380			1152
	att caa tta aat acg tta gcc atg tat ggt ttg gaa aag ttc ttc tca Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser 385 390 395 400			1200
	aga att gag aga gta aaa atg tta caa acg tgg ggt ggt ata cca tca Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser 405 410 415			1248

	atg cta cca aag gga gaa gag gtc att tgg ggg gat atg aag tca tct Met Leu Pro Lys Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser	1296
	420 425 430	
5	tca gag gat gca ttg aat aac aac act gac aca tac ggc aat ttc att Ser Glu Asp Ala Leu Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile	1344
	435 440 445	
10	cga ttt gaa agg aat acg agc gat gct ttc aac aaa aat ttg aca atg Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met	1392
	450 455 460	
15	aaa gac gcc att aac atg aca tta tcg ata tca cct gaa tgg ctc caa Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln	1440
	465 470 475 480	
20	aga aga gta cat gag cag tad tcg ttc ggc tat tcc aag aat gaa gaa Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu	1488
	485 490 495	
25	gag tta aga aaa aat gag cta dac cac aag cac tgg tcg aat cca atg Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met	1536
	500 505 510	
30	gaa gta cca ctt cca gaa gct ccc cac atg aaa atc tat tgt ata tac Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr	1584
	515 520 525	
35	ggg gtg aac aac cca act gaa agg gca tat gta tat aag gaa gag gat Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp	1632
	530 535 540	
40	gac tcc tct gct ctg aat ttg acc atd gac tac gaa agc aag caa cct Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro	1680
	545 550 555 560	
45	gta ttc ctc acc gag ggg gac gga acc gtt ccg ctc gtg gcg cat tca Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser	1728
	565 570 575	
50	atg tgt cac aaa tgg gcc cag ggt gct tca ccg tac aac cct gcc gga Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly	1776
	580 585 590	
55	att aac gtt act att gtg gaa atg aaa cac cag cca gat cga ttt gat Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp	1824
	595 600 605	
60	ata cgt ggt gga gca aaa agc gcc gaa cac gta gac atc ctc ggc agc Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser	1872
	610 615 620	
65	gcg gag ttg aac gat tac atc ttg aaa att gca agc ggt aat ggc gat Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp	1920
	625 630 635 640	
70	ctc gtc gag cca cgc caa ttg tct aat ttg agc cag tgg gtt tct cag Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln	1968
	645 650 655	

1986

atg ccc ttc cca atg taa
Met Pro Phe Pro Met
660

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<212> PRT
<213> *Saccharomyces cerevisiae*

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15 Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
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Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
35 40 45

20 Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
50 55 60

25 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
65 70 75 80

Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
85 90 95

30 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
100 105 110

Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
115 120 125

35 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
130 135 140

40 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
145 150 155 160

Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
165 170 175

45 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
180 185 190

Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
195 200 205

50 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
210 215 220

Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
55 225 230 235 240

Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
245 250 255

60 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
260 265 270

Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
 275 280 285

5 Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
 290 295 300

Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
 305 310 315 320

10 Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
 325 330 335

Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val
 15 340 345 350

Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly
 355 360 365

20 Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
 370 375 380

Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
 385 390 395 400

25 Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
 405 410 415

Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
 30 420 425 430

Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
 435 440 445

35 Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
 450 455 460

Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
 465 470 475 480

40 Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
 485 490 495

Glù Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
 45 500 505 510

Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
 515 520 525

50 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
 530 535 540

Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
 545 550 555 560

55 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
 565 570 575

Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
 60 580 585 590

Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
595 600 605

5 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
610 615 620

Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
625 630 635 640

10 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
645 650 655

Met Pro Phe Pro Met
15 660

SEQUENCE LISTING

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<211> 1986

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gat gaa aac aat aaa ggg ggt tct gat cat aac aag cga gag agc aga 96
Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
20 25 30

aac cac att cat cat caa cag gga tta ggc cat aag aga aga agg ggt 144
Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
35 40 45

att agt ggc agt gca aaa aga aat gag cgt ggc aaa gat ttc gac agg 192
Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
50 55 60

aaa aga gac ggg aac ggt aga aaa cgt tgg aga gat tcc aga aga ctg 240
Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
65 70 75 80

att ttc att ctt ggt gca ttc tta ggt gta ctt tgg ccg ttt agc ttt 288
Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
85 90 95

ggc gct tat cat gtt cat aat agc gat agc gac ttc ttt gac aac ttt 336
Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
100 105 110

gta aat ttt gat tca ctt aaa gtg tat ttg gat gat tgg aaa gat gtt 384
 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
 115 120 125

ctc cca caa ggt aca agt tcg ttt acc gat gat att cag gct ggt aac 432
 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
 130 135 140

tac tcc aca tct tcc tta gat gat ccc agt gaa aat ttt gcc gtt ggt 480
 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
 145 150 155 160

aaa caa ctc tta cgt gat tat aat acc gag gcc aaa cat ccc yll yea 520
 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
 165 170 175

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 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
 180 185 190

gga gac gat gag tgc gat agr tct gcg cat ttt cgt aaa cgg ctg tgg 624
 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
 195 200 205

gga agt ttt tac atg ctg aga aca aca atg gtt atg gat aaa gtt tgt tgg 672
 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
 210 215 220

ctg aaa cat gta atg tta gat cct gaa aca ggt ctg gac cca ccg aac 720
 Ieu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
 225 230 235 240

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 Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
 245 250 255

gca ggg tat tgg att tgg aac aaa gtt ttc caa aat ctg gga gta att 816
 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
 260 265 270

ggc tat gaa ccc aat aaa atg acg agt gct gcs tat gat tgg agg ctt 864
 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
 275 280 285

gca tat tta gat cca gaa aga cgc gat agg tac ttt acg aag cta aag 912
 Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
 290 295 300

gaa caa atc gaa ctg tt cat caa ttg agt ggt gaa aaa gtt tgt tta 960
 Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
 305 310 315 320

act gga cat tct atg ggt tct cag att atc tt tac tt atg aag tgg 1008
 Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
 325 330 335

gtc gag gct gaa ggc cct ctt tac ggt aat ggt cgt ggc tgg gtt 1056
 Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Arg Gly Trp Val
 340 345 350

aac gaa cac ata gat tca ttc att aat gca gca ggg acg ctt ctg ggc 1104
 Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly
 355 360 365

gct cca aag gca gtt cca gct cta att agt ggt gaa atg aag gat acc 1152
 Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
 370 375 380

att caa tta aat acg tta gcc atg tat ggt ttg gaa aag ttc ttc tca 1200
 Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
 385 390 395 400

aga att gag aga gta aaa atg tta caa acg tgg sgt ggt ata cca tca 1248
 Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
 405 410 415

atg cta cca aag gga gaa gag gtc att tgg sgg gat atg aag tca tct 1296
 Met Leu Pro Lys Gly Glu Val Ile Trp Gly Asp Met Lys Ser Ser
 420 425 430

tca gag gat gca ttg aat aac aac act gac aca tac ggc aat ttc att 1344
 Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
 435 440 445

cga ttt gaa agg aat acg agc gat gct ttc aac aaa aat ttg aca atg 1392
 Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
 450 455 460

aaa gac gcc att aac atg aca tta tcg ata tca ccc gaa tgg ctc caa 1440
 Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
 465 470 475 480

1488

aga aga gta cat gag cag tac tcg ttc ggc tat tcc aag aat gaa gaa
Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
485 490 495

1536

gag tca aga aaa aat gag gta cac cac aag cac tgg tcg aat cca atg
Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
500 505 510

1584

gaa gta cca ctt cca gaa gct ccc cac atg aaa atc tat tgt ata tac
Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
515 520 525

1632

ggg stg aac aac cca act gaa agg gca tat gta tat aag gaa gag gat
Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
530 535 540

1680

gac tcc tct gct ctg aat ttg acc acc gac tac gaa aig aag caa cct
Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
545 550 555 560

1728

gta ttc ctc acc gag ggg gac gga acc gtt ccg ctc gtg gcg cat tca
Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
565 570 575

1776

atg tgt cac aaa cgg gcc cag ggt gct tca ccg tac aac cct gcc gga
Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
580 585 590

1824

att aac gtt act att ttg gaa atg aaa cac cag cca gat cga ttt gat
Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
595 600 605

1872

ata cgt ggt gga gca aaa agc gcc gaa cac gta gac atc ctc ggc agc
Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
610 615 620

1920

scg gag ttg aac gat tac atc ttg zaa att gca agc ggt aat ggc gat
Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
625 630 635 640

1968

ctc gtc gag cca cgc caa ttg tct aat ttg agc cag tgg gtt tct cag
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645 650 655

1986

atg ccc ttc cca atg taa
Met Pro Phe Pro Met
660

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Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
35 40 45
Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
50 55 60
Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
65 70 75 80
Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
85 90 95
Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
100 105 110
Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
115 120 125
Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
130 135 140
Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
145 150 155 160
Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
165 170 175
Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
180 185 190
Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
195 200 205
Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
210 215 220
Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
225 230 235 240
Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
245 250 255
Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
260 265 270
Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
275 280 285
Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
290 295 300
Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
305 310 315 320

Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
 325 330 335
 Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val
 340 345 350
 Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly
 355 360 365
 Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
 370 375 380
 Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
 385 390 395 400
 Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
 405 410 415
 Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
 420 425 430
 Ser Glu Asp Ala Leu Asn Asn Asn Asp Thr Tyr Gly Asn Phe Ile
 435 440 445
 Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
 450 455 460
 Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
 465 470 475 480
 Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
 485 490 495
 Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
 500 505 510
 Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
 530 535 540
 Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
 545 550 555 560
 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
 565 570 575
 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
 580 585 590
 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
 595 600 605
 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
 610 615 620
 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
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ACCAAAACAA	AACTAACCA	TTTCTGAA	TTTCATATT	AGGAGTAGTC	3200
GTGCTTTAA	AAAATTGTT	TTAAGAATCC	GAAGAACTAG	TTCATATCTT	3250
GATTGTGCAA	TATCTGCAGG	TCTGGAAC	TGGTGTGATGG	GAACGCTGGA	3300
CCATATACTG	GGGATGAGAC	GGTAAGCTCA	GAAGTTGGTT	TTGAAATTAT	3350
CTTCVTCGAA	ACTACTGAAG	ACTAAGATAA	TACTTGCTTC	TGGAACACTG	3400
CTTGTATGT	TCTCTAGTAC	ACTGCAATAT	TGACTCTCCG	CTACTTTTAT	3450
TGATTATGAA	ATTGATCTCT	TATAGGTACG	CTATCATTCA	CTCTCTTGGT	3500
GCAAGAATTG	GCTCGGACCT	AAAGTTAACAA	TAACAATGGC	TCCCCAGGTA	3550
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TCTCTGTACT	CCTCAAGAAC	TTGTATTAAT	CTAAACGAGA	TTCTCATTCG	3700
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TAAATGTTGA	TCATGAGCAT	GGGTCAAGACA	TCATAGCTAA	CATGACAAAAA	3800
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 <212> cDNA
 <213> tomato
 <400> 11

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AGGATTCTGA AAGTTTCCA GGGACAGAGAA CAGCAGTTG GGAGCTTGAT	200
AAGCAATTC ACAGGAACAT TGTCAGACT CCAGCTTGA TGCAGGAGCT	250
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TTACAAAAGG TGGTGTCTGA TCCTCACTAT TTTCTTCTAT AAATGTTGA	350
GTTTGTATTG ACATTGTAAG TATTGCAACA AAAAGCAAAG CGTGGGCCTC	400
TGAGGGATCA GGACTGCTAT TCGGATTACG GGAAAGCTCG ATGTGCATGG	450
GCTGAACATT GTGAATACAG GTTAGAATAT TCAATTATA TTTTGCAGAA	500
TATTCTCTTT TTGTGTATTG AGGCCACCTT TCCCCGGTCA CAACGATGCA	550
GATATGTATT CGGGGATGTT CACCTGGGAC AGAGTTGCAG ATTGAAGAGT	600
TCTACATCTC ACATCCTGTC ACACTATGTG TGATATTTAA GAAACTTGT	650
TTGGCGGAAC AACAAAGTTG CACAAACATT TGAAGAAGAA AGCGAAATGA	700
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